Automated Reconstruction and Comparison of Metabolic Models for Diverse Fungal Genomes.

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Fungal genome-scale metabolic models are an efficient way of predicting phenotypes across various environmental conditions. However, automating the construction of high-quality fungal models has been a challenge. Here we introduce a methodology to construct genome-scale fungal models in

an automated fashion based on a curated set of reactions that are derived from 14 published fungal metabolic models. As the basis for the method, we produced a fungal model template that encompasses the biochemistry data from the published fungal models and the structural annotations from the associated fungal genomes.

Our approach uses structural annotations of any user-submitted fungal genome and computes a set of orthologous proteins against the curated fungal template in order to assert the presence or absence of specific biochemical reactions and pathways. Once the orthologous protein families are determined, the related biochemistry data is propagated to construct a new draft metabolic model. This method is deployed in the Department of Energy Systems Biology Knowledgebase (KBase) (https://narrative.kbase.us/) as an app called “Build Fungal Model”. We applied this new app to construct draft fungal models for more than 100 fungal genomes imported from Joint Genome Institute (JGI) MycoCosm resource (https://genome.jgi.doe.gov/programs/fungi/index.jsf). We compared these models side-by-side, exploring how each genome overlaps with our curated model template and plotting model variance along the phylogenetic tree of fungal genomes. All draft fungal models are available for download by a KBase Narrative.